

Fig. 1

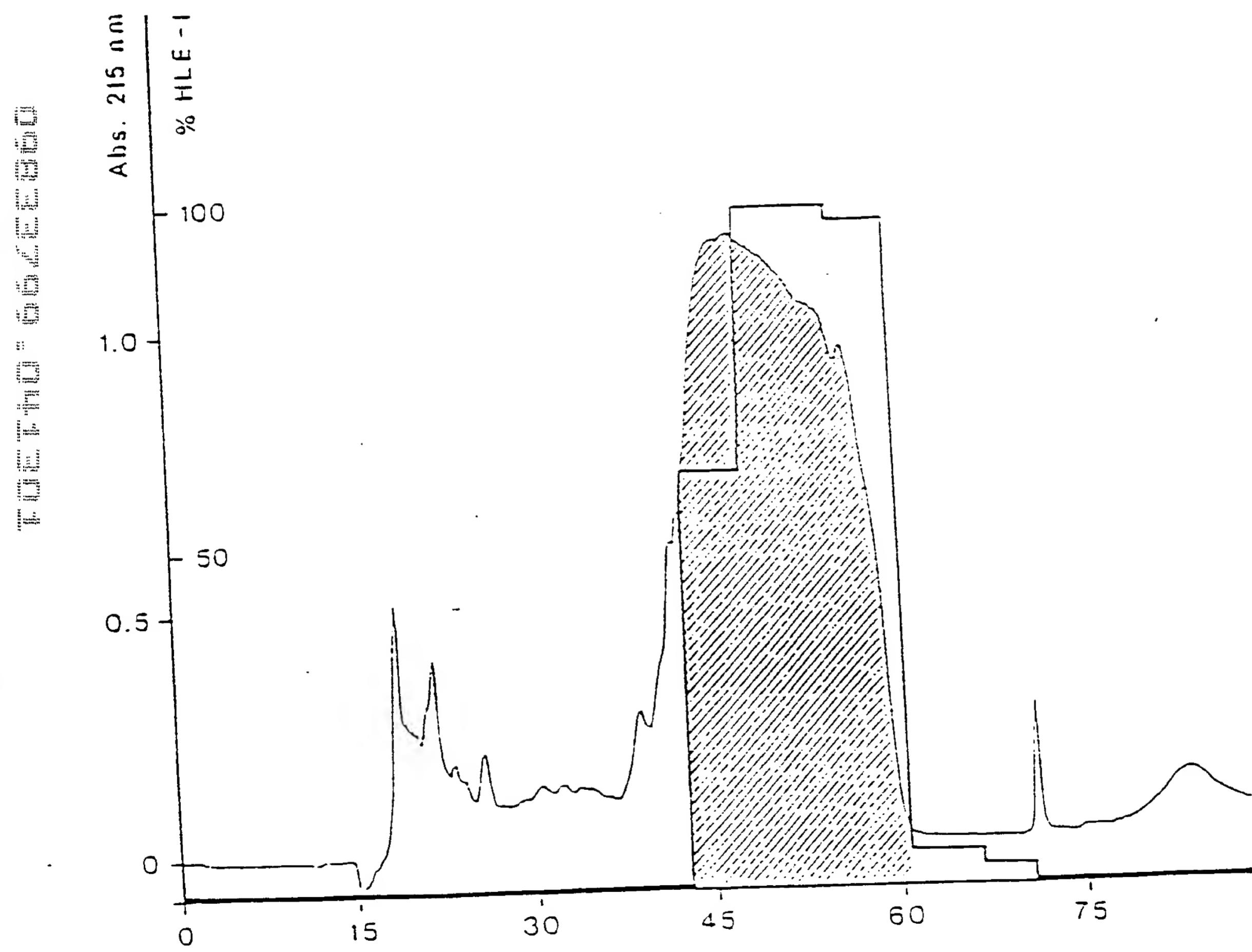


Fig. 2

"W. L. BRADLEY" = "W. L. BRADLEY"

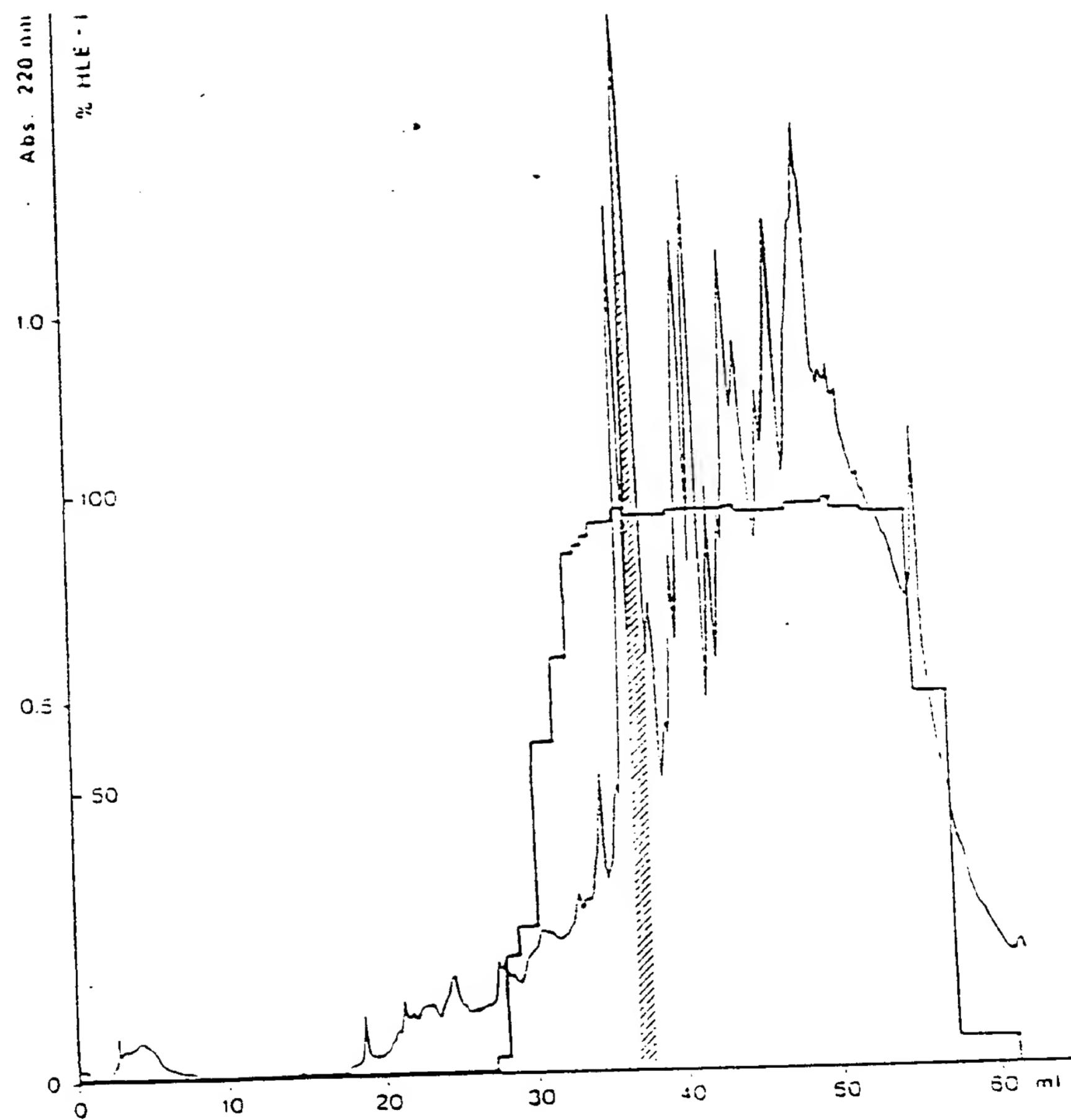


Fig. 3

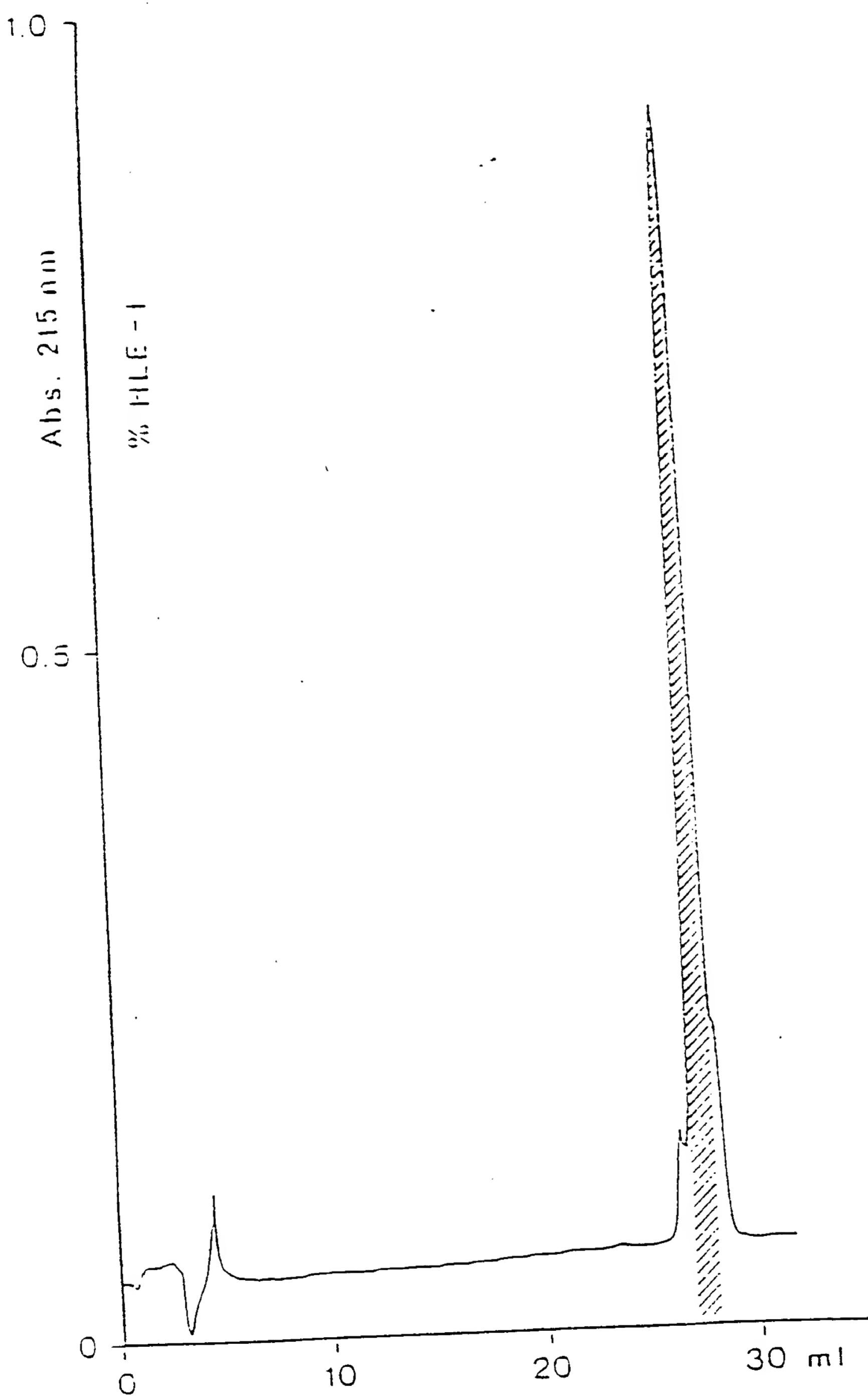


Fig. 4

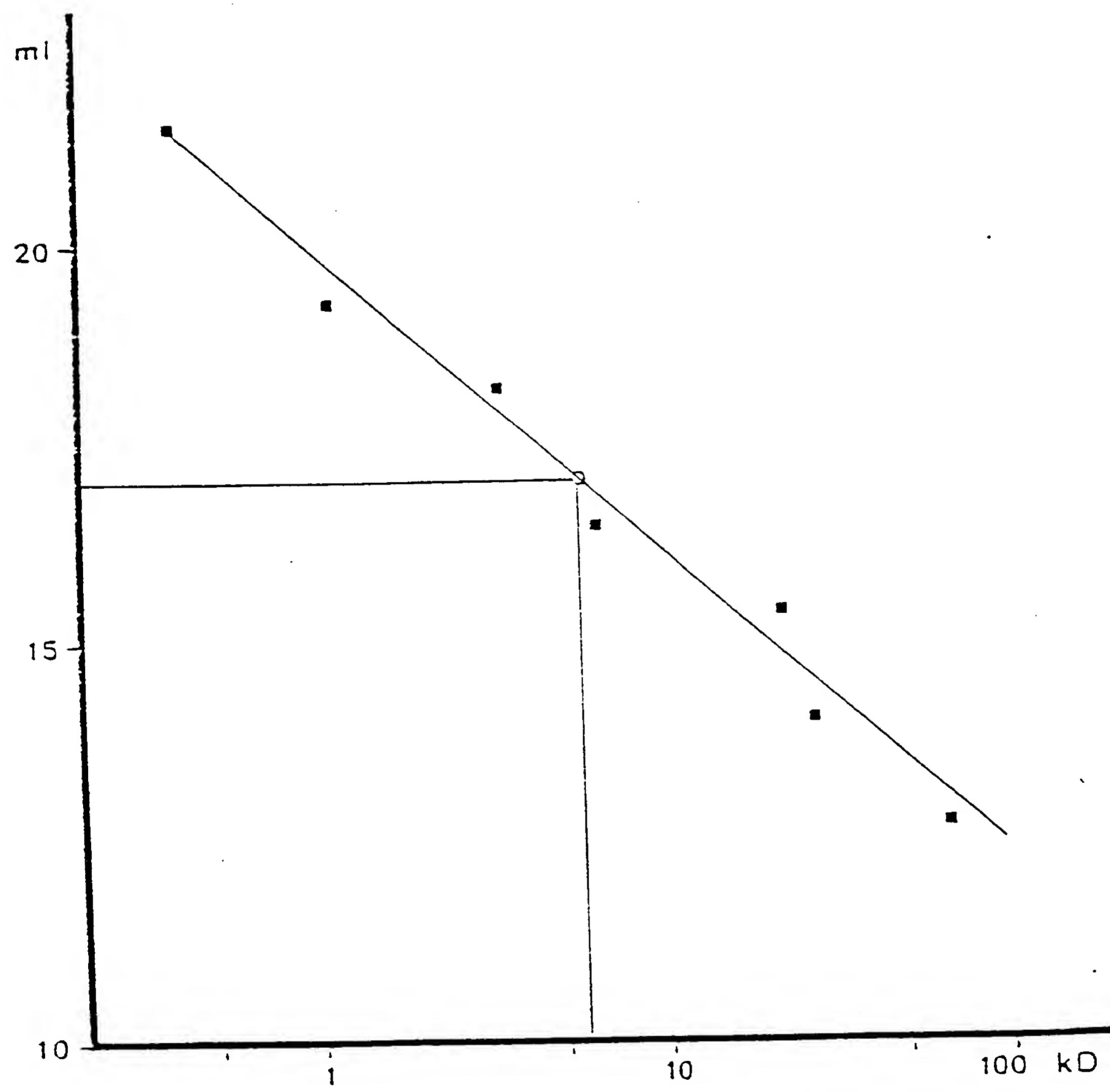


Fig. 5

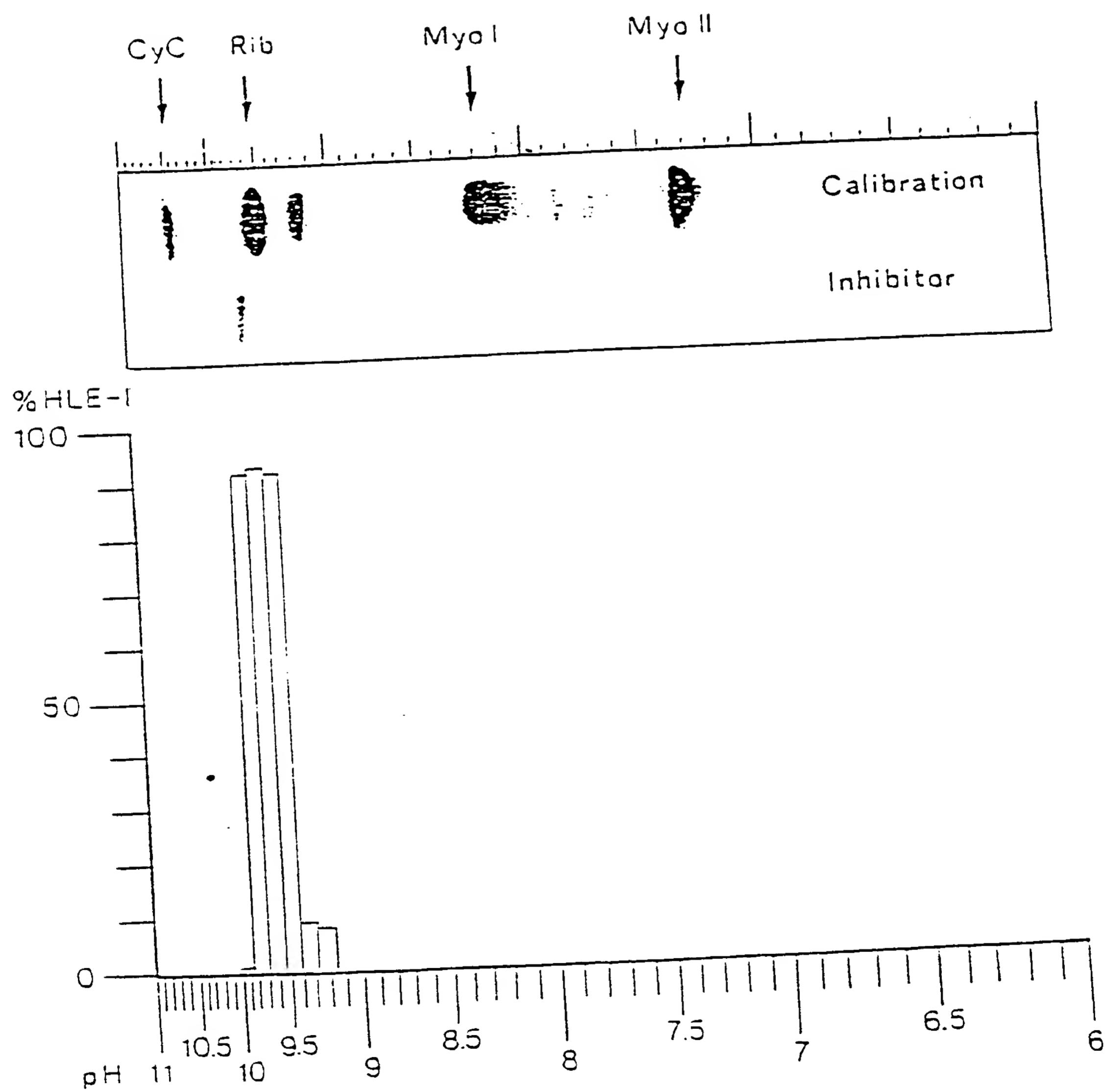


Fig. 6

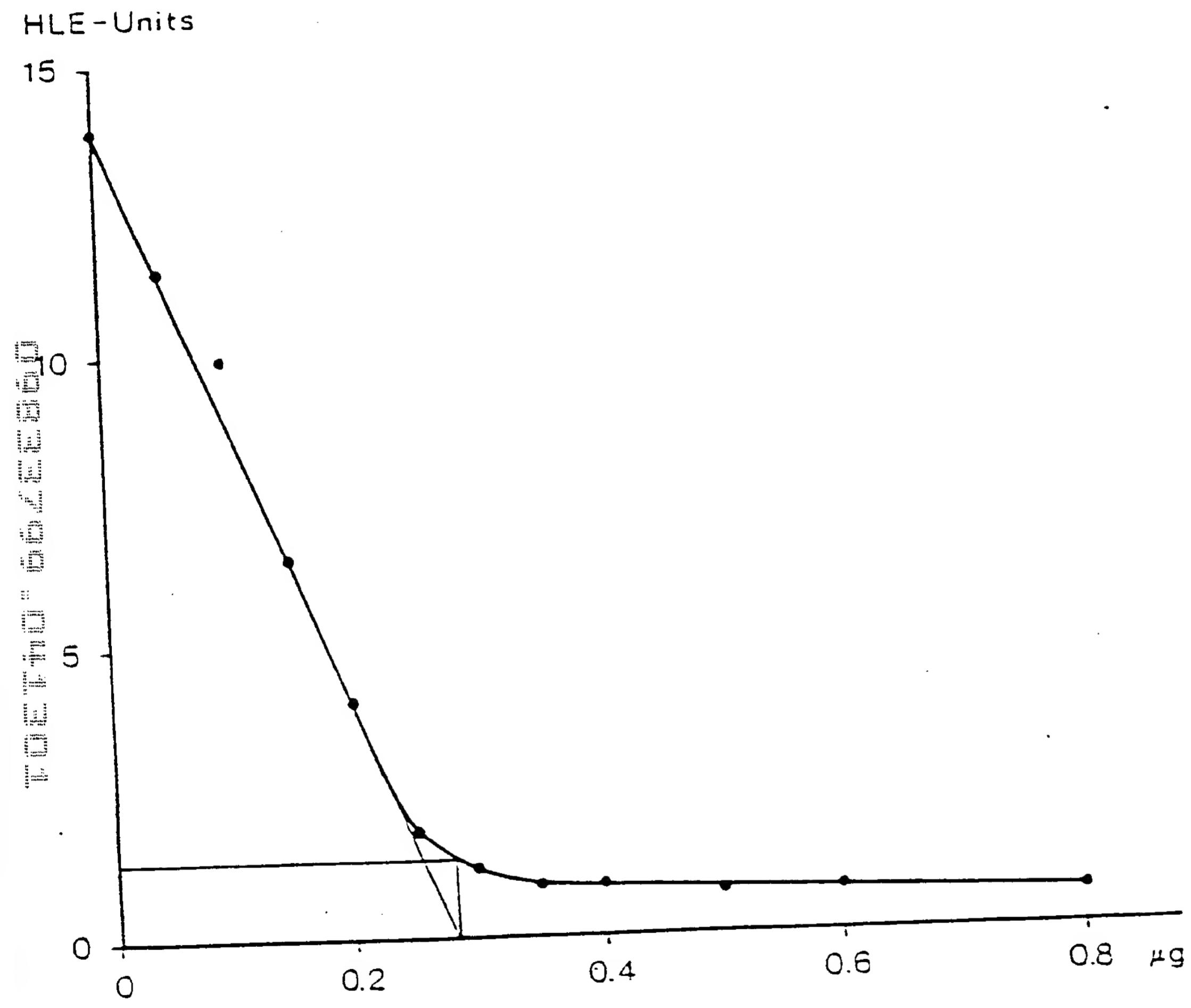


Fig. 7

FIGURE 8

PROTEIN SEQUENCE OF ELASTASE INHIBITOR

1 Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys

DIRECT SEQUENCE ————— T10 —————

Pro Gly Ser Cys Pro Ile Ile Leu Ile Arg Cys Pro

———— T6 —————

Met Leu Asn Pro Pro Asn Arg Cys Leu Lys Asp Thr

———— T6 —————

Asp Cys Pro Gly Ile Lys Cys Cys Glu Gly Ser

———— C2-6 —————

———— C3-9 —————

———— C2-6 —————

———— C3-9 —————

Cys Gly Met Ala Cys Pro Val Pro Val Pro 57Gln

———— T6 —————

———— C2-3 —————

———— C2-5 —————

X=UNIDENTIFIED T=TRYPTIC FRAGMENTS C=CHYMOTRYPTIC FRAGMENTS

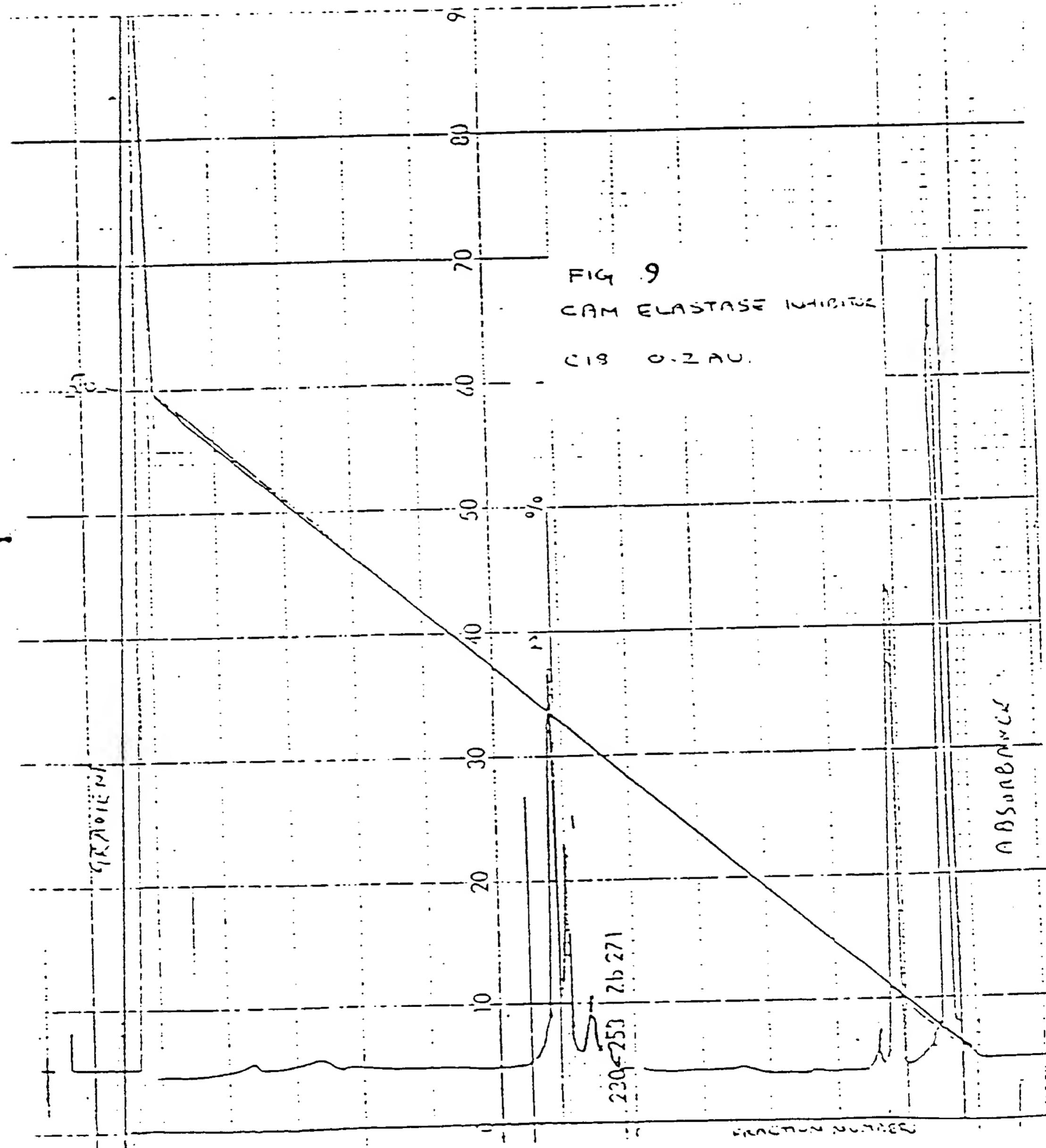


FIG. 9

FIG 10

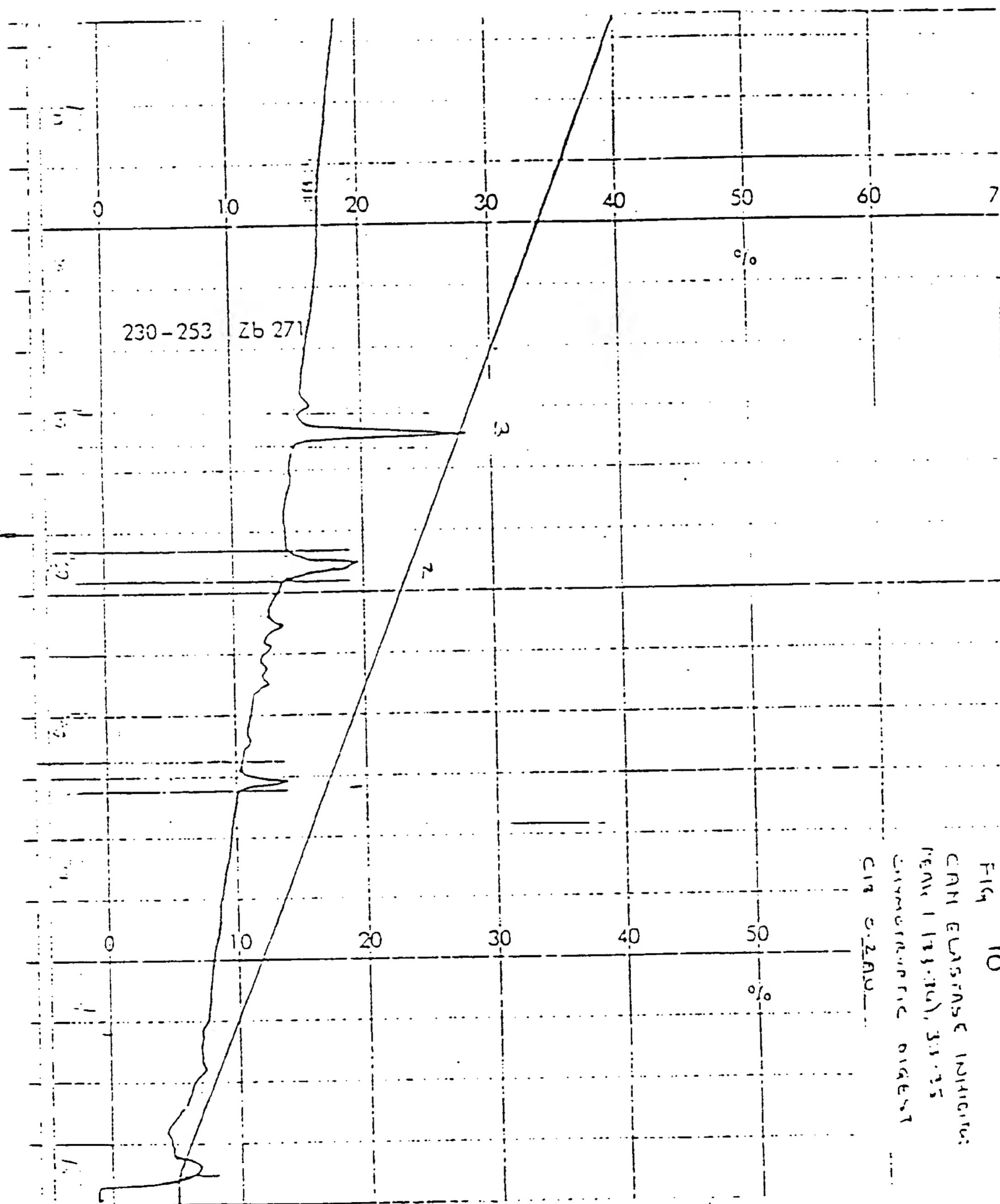


FIG 10
CAN EMISSIVE INDICATIVE
OF THE ZB 271, 230-253
STRUCTURE

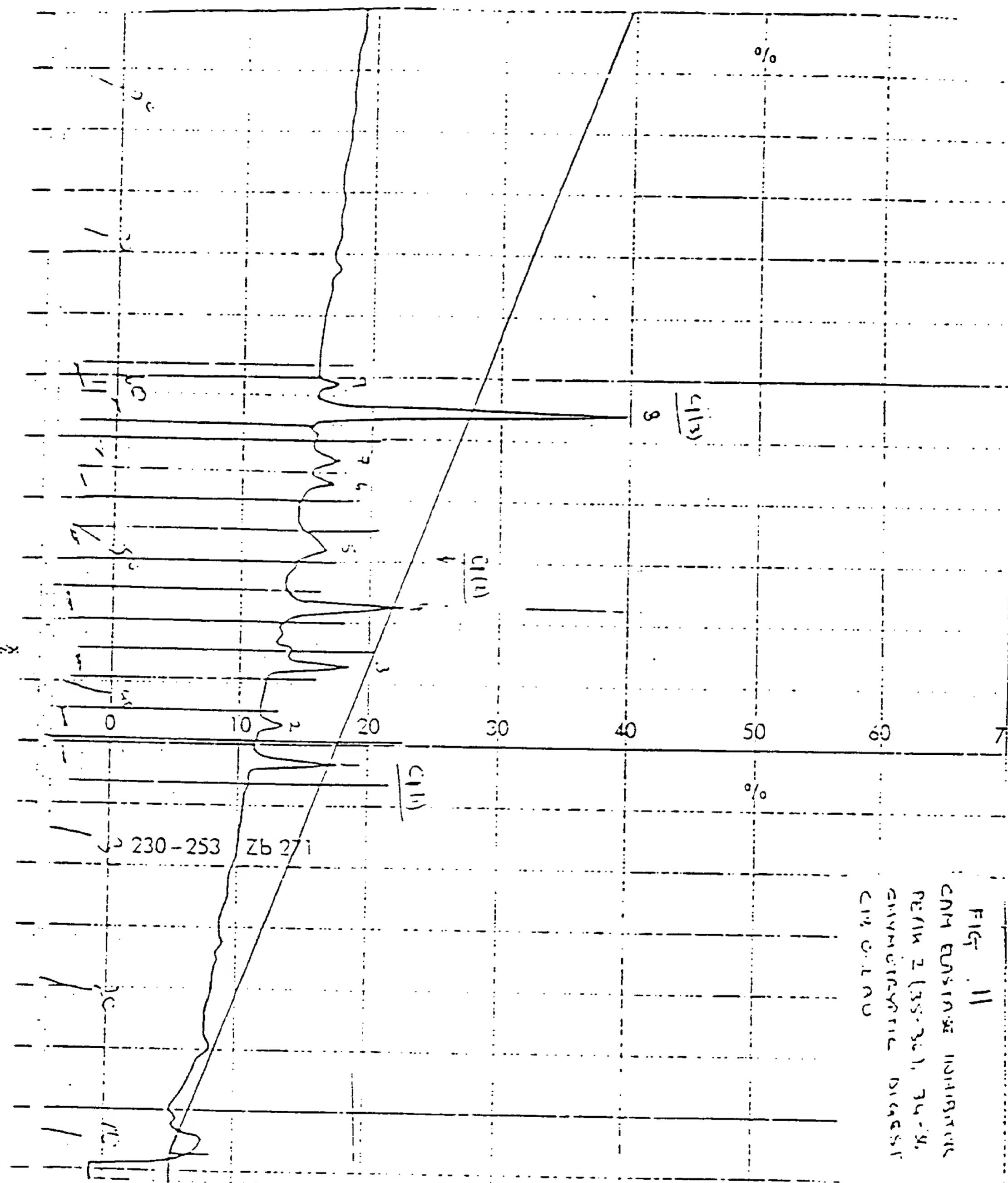


FIG 11

FIG 11
C11/C10 vs θ
Ratio of 230-253, Zb
271 cm⁻¹ bands
versus angle of incidence

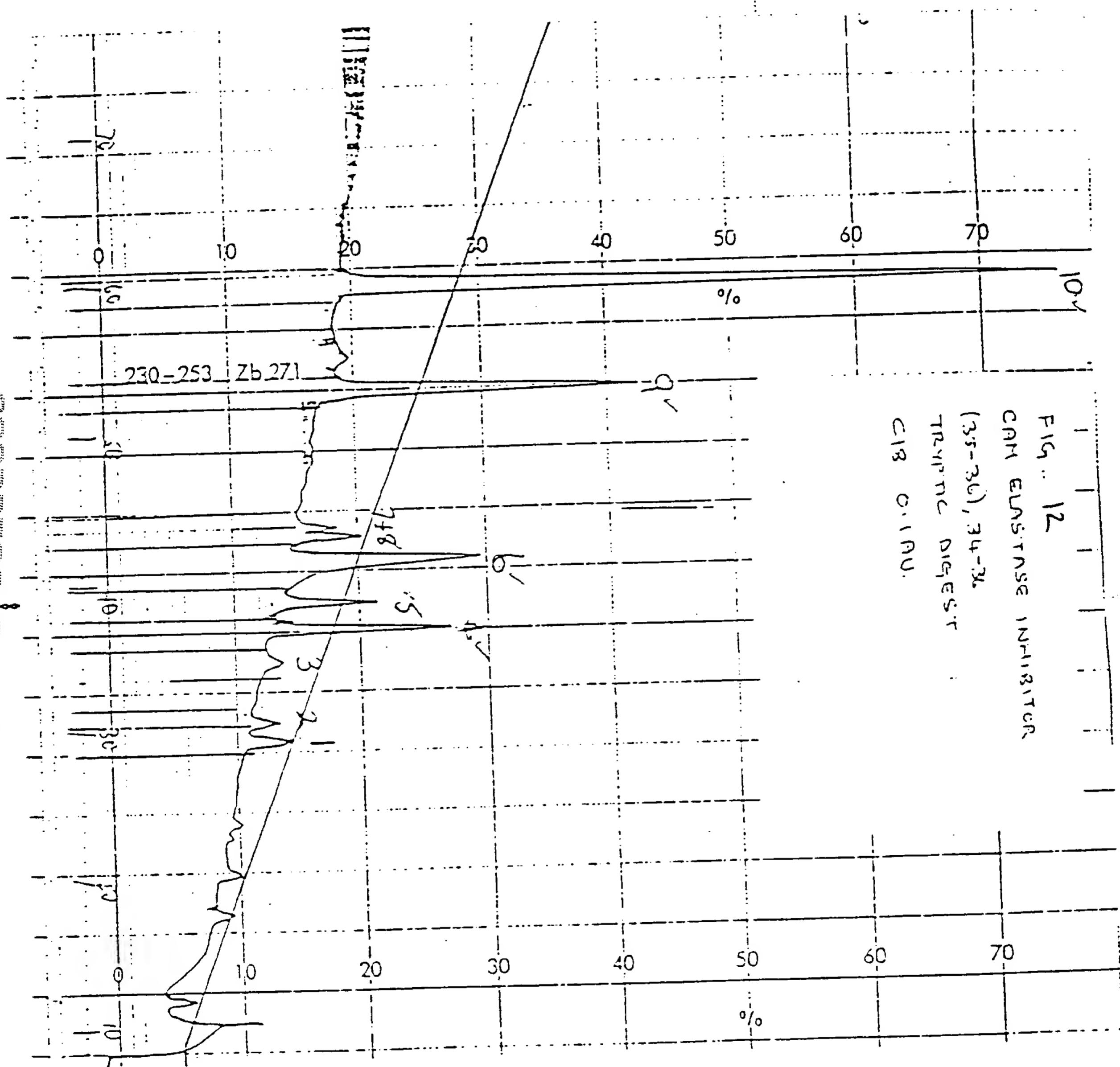


FIG. 12
CAN ELASTASE INHIBITOR
(35-36), 34-35
TRYPTIC DIGEST
C18 O.1AU.

FIG 12

Figure 13

AlaGlnGluProValLysGlyProValSerThr

1 → ELI1
 AATTGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAAGTTAAAGGTCTGTCTACT
 GCTCGAGCCATGGTATGGACGTATACGAGTTCTGGTCAATTCCAGGACACAGATGA

63 → ELI3
 AAGCCAGGTTCTTGTCTTATTATCTTGAATTGATTGTTGCGCTATGTTAAACCCACCTAACCGT
 TTCCGGTCCAGAACAGGATAATAGAACTAACGCAACCGCGATAACAATTGGGTGGATTGGCA
 ELI2 ←

123 → ELI5
 TGTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGTGAAGGTTCTGCGGTATG
 ACAAAACTTCTGTGACTAACAGGTCCATAGTTTACGACACTTCCAAGGACGCCATAC
 ELI4 ←

183 AlaCysPheValProGlnEndEnd
 GCTTGTTCGTTCCACAATAATAG

CGAACAAAGCAAGGTGTTATTATCCTAG 210
 ELI6 ←

Figure 14

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys
GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC

5' DNA

Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys
CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln
TGC GGG ATG GCC TGT TTC GTT CCC CAG

Z = T, C or A

P = A or G

Figure 15

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys
 GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC

5' DNA

Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys
 CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln

TGC GGG ATG GCC TGT TTC GTT CCC CAG TAG GAGGGAGCCGGTCCCTGCTGCACCTGT

GCCGTCCCCAGAGCTACAGGCCCATCTGGTCCTAAGTCCCTGCTGCCCTCCCTCCACACTGTCCA
 TTCTTCCTCCATTCAAGGATGCCACGGCTGGAGCTGCCCTCTCATCCACTTCCAAAAGAGTTCCG

Poly A 3'

signal

Z = T, C or A

P = A or G

FIGURE 16

Cont'd 16b of 19

FIGURE 16 CONTINUED

190

210

230

AGTCTCCACTAACGCCTGGCTCCTGCCCLATTATCTTGTCCGGTGCATGTTGAATCC
 oValSerThrLysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnPr

250

270

290

CCCTAACCGCTGCTTGAAAGATACTGACTGCCAGGAATCAAGAAGTGCTGTGAAGGCTC
 oProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySe

310

330

350

TTGCGGGATGGCCTGTTGTTCCCCAGTGAGAGGGAGCCGGTCCTTGCTGCACCTGTGC
 rCysGlyMetAlaCysPheValProGlnEnd

370

390

410

CGTCCCCAGAGCTACAGGCCCATCTGGCTTAAGTCCCTGCTGCCCTTCCCCTTCCCAC

430

450

470

ACTGTCCATTCTCCTCCCATTCAAGGATGCCACGGCTGGAGCTGCCTCTCTCATCCACT

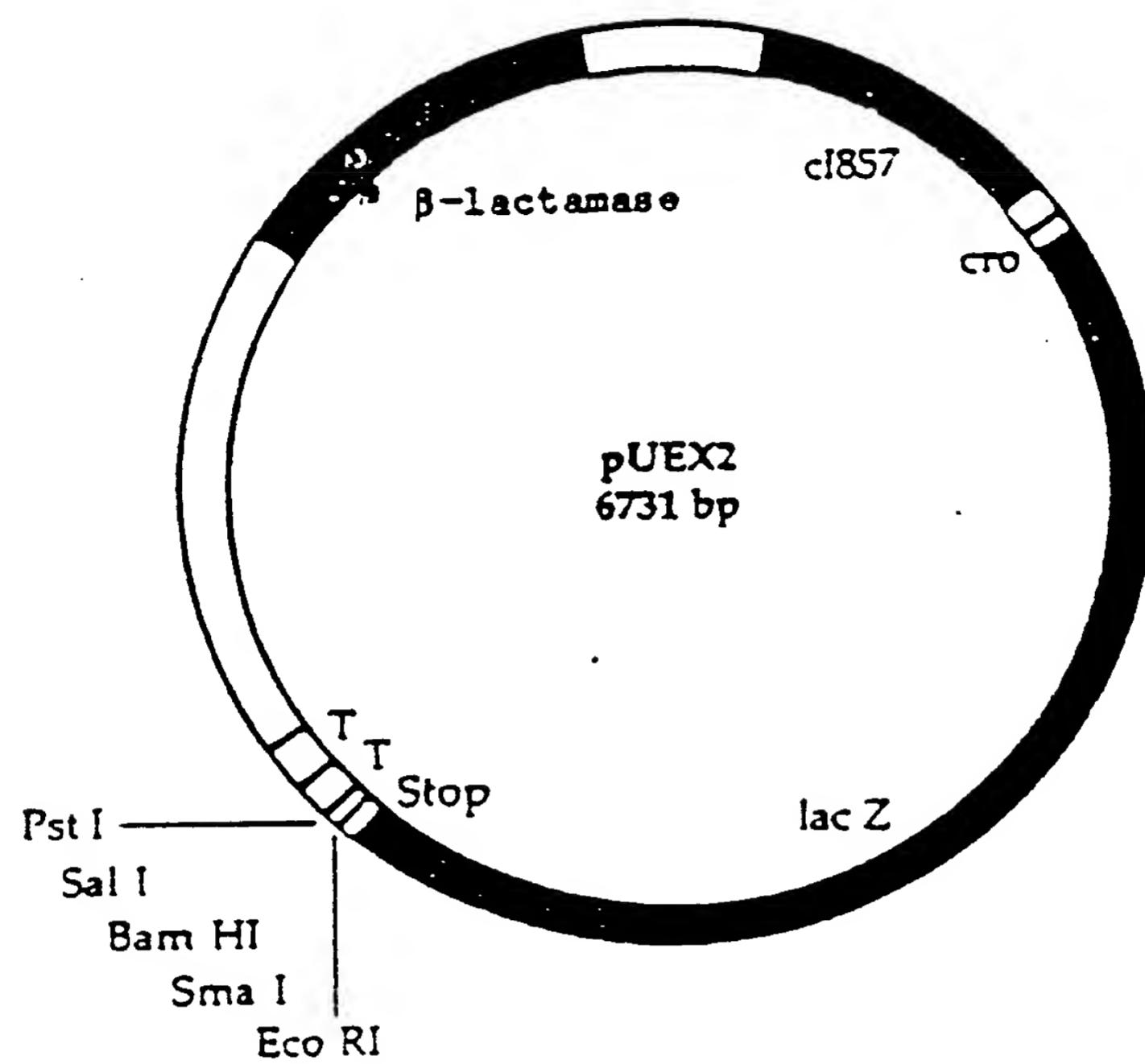
490

TTCCAATAAGAGTTCCGGAATT

Poly A
signal

EcoRI

EcoRI Poly A signal



pUEX2 EcoRI SmaI BamHI SalI PstI
 | | | | |
 GAA TTC CCG GGG ATC CGT CGA CCT GCA GCC AAG CTT GCT GAT TGA
 Glu Phe Pro Gly Ile Arg Arg Pro Ala Ala Lys Leu Ala Asp ***

FIG 17

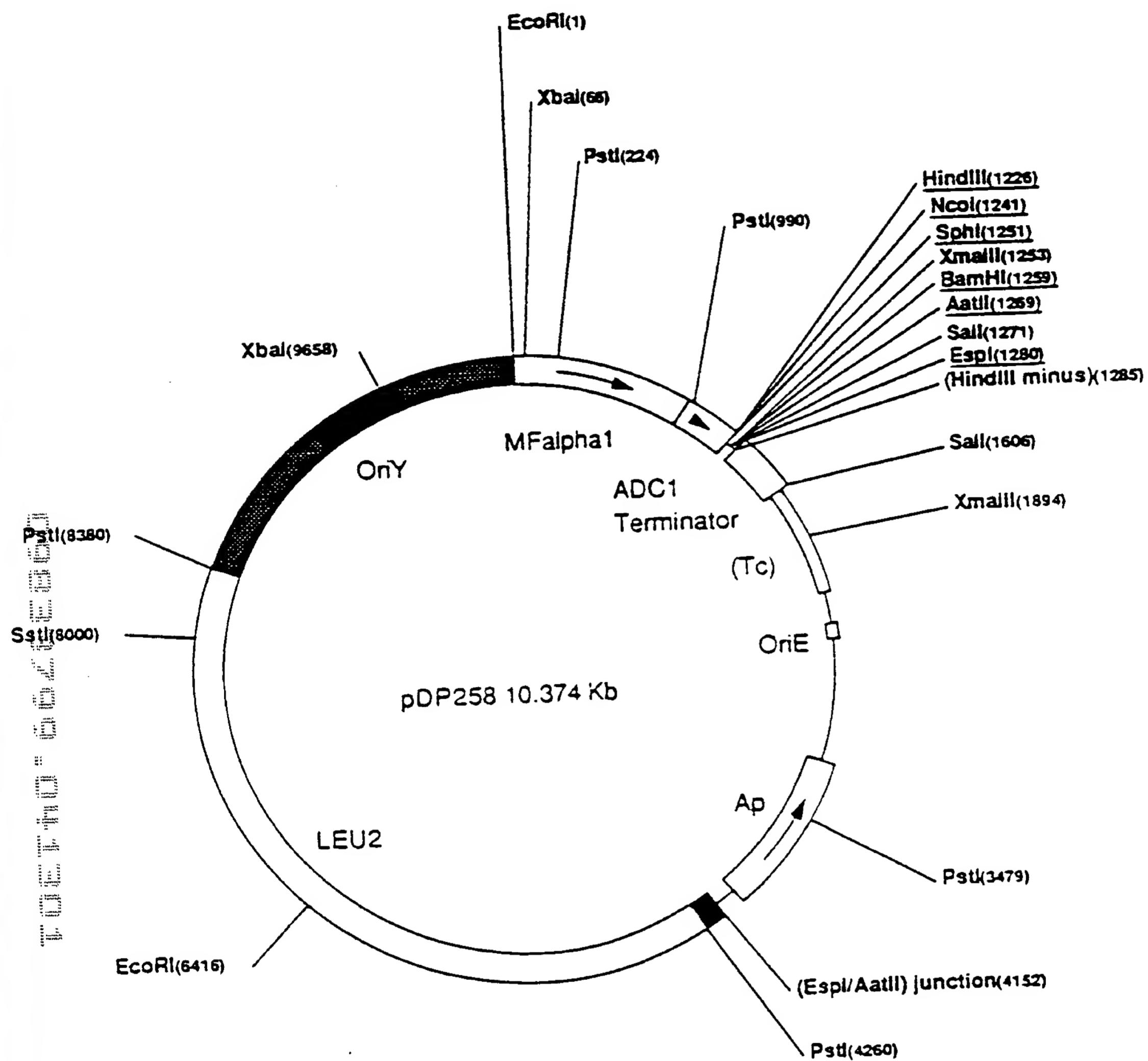


FIG 18

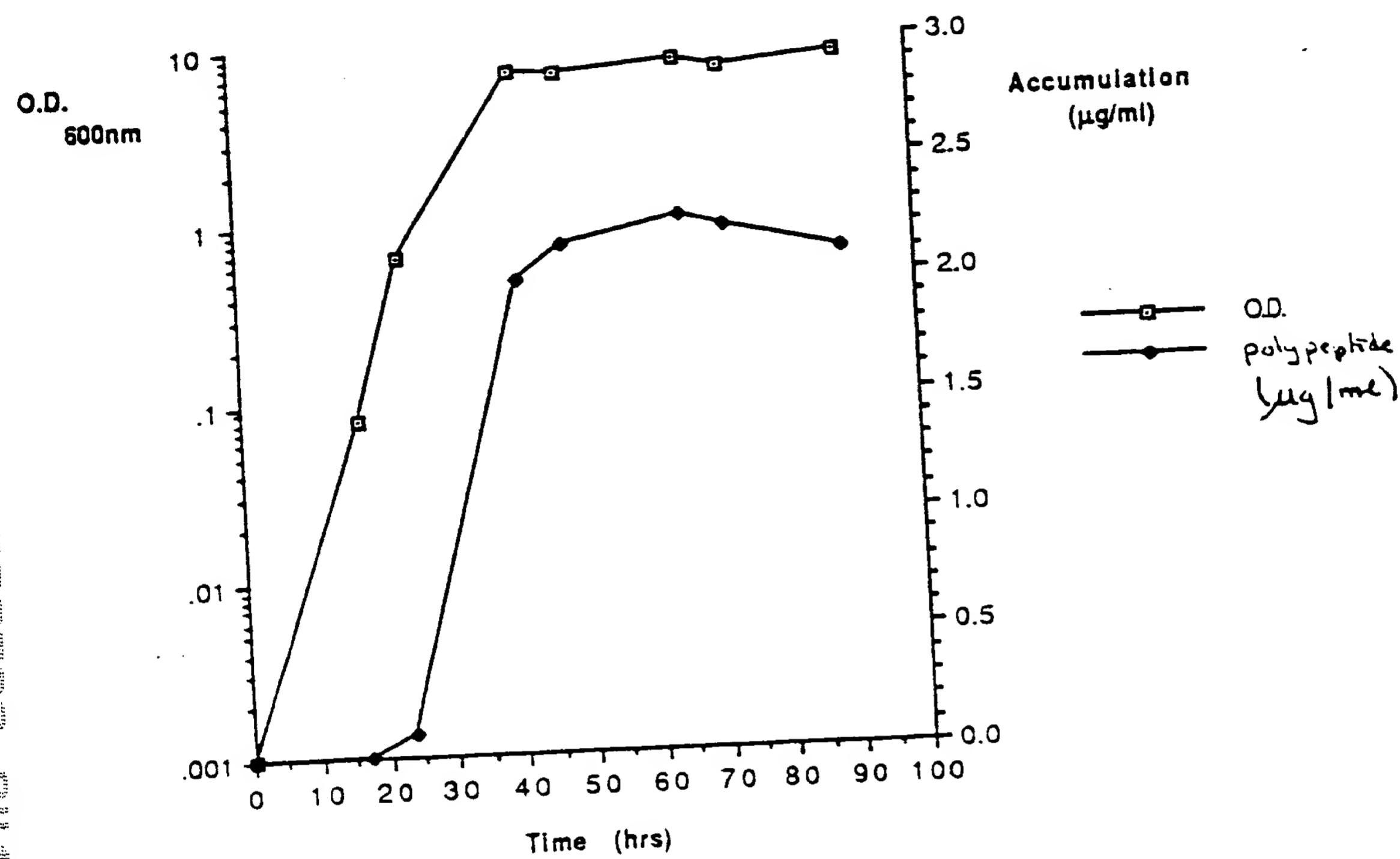


FIG 19